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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/020,419

DATE: 05/09/2002  
TIME: 14:27:34

Input Set : A:\P2637-1(US).txt  
Output Set: N:\CRF3\05092002\J020419.raw

3 <110> APPLICANT: Goddard,Audrey  
4 Wood,William I.  
5 Ye,Weilan  
6 Zhang,Zemin  
8 <120> TITLE OF INVENTION: NOVEL SECRETED POLYPEPTIDE AND METHODS OF TREATMENT OF  
9 BONE DISORDERS  
11 <130> FILE REFERENCE: P2637-1(US)  
13 <140> CURRENT APPLICATION NUMBER: US 10/020,419  
14 <141> CURRENT FILING DATE: 2001-12-13  
16 <150> PRIOR APPLICATION NUMBER: US 60/132,379  
17 <151> PRIOR FILING DATE: 1999-05-04  
19 <150> PRIOR APPLICATION NUMBER: PCT/US00/05601  
20 <151> PRIOR FILING DATE: 2000-03-01  
22 <150> PRIOR APPLICATION NUMBER: PCT/US01/19692  
23 <151> PRIOR FILING DATE: 2001-06-20  
25 <150> PRIOR APPLICATION NUMBER: PCT/US01/21735  
26 <151> PRIOR FILING DATE: 2001-07-09  
28 <160> NUMBER OF SEQ ID NOS: 4  
30 <210> SEQ ID NO: 1  
31 <211> LENGTH: 999  
32 <212> TYPE: DNA  
33 <213> ORGANISM: Homo Sapien  
35 <400> SEQUENCE: 1  
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38 gtgctgtgc tgctcctggc gggagccccc gccgcgcggc ccactcccc 100  
40 gacctgtac tcccgcatgc gggccctgag ccagagatc acccgcgact 150  
42 tcaacctcct gcaggctctcg gagccctcgg agccatgtgt gagataacctg 200  
44 cccaggctgt acctggacat acacaattac tgtgtgctgg acaagctgcg 250  
46 ggactttgtg gcctogcccc cgtgttggaa agtgcccaag gtagattct 300  
48 tgaaggacaa agcacggaag ctgtacacca tcatgaactc gttctgcagg 350  
50 agagatttgg tattctgtt ggtgactgc aatgccttgg aatacccaat 400  
52 cccagtgtact acggctctgc cagatcgta ggcctaagg aactgagacc 450  
54 agagaaaagaa cccaagagaa ctaaagttagt gtcagctacc cagacttaat 500  
56 gggccagagc catgaccctc acaggtctg ttttagttgt atctgaaact 550  
58 gttatgtatc tctctacctt ctggaaaaca gggctggat tcctaccagg 600  
60 gaacctcctt tgagcataga tttagcaacc atgcttctca ttcccttgac 650  
62 tcatgtcttg ccaggatgtt tagatacaca gcatgttgat ttggtcacta 700  
64 aaaagaagaa aaggactaac aagttcaact tttatgaaca actatttga 750  
66 gaacatgcac aatgtatgt ttttattact ggttaatgg agtaatggta 800  
68 cttttattct ttcttgatag aaacctgctt acatttaacc aagcttctat 850  
70 tatgccttt tctaacacag actttcttca ctgtcttca tttaaaaaga 900  
72 aattaatgtc cttaagatata tattttacg tagtgcgtac aggacccact 950  
74 ctttcattga aaggtgatga aaatcaaata aagaatctct tcacatgga 999

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76 <210> SEQ ID NO: 2  
77 <211> LENGTH: 136  
78 <212> TYPE: PRT  
79 <213> ORGANISM: Homo Sapien  
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83 1 5 10 15  
85 Gly Ala Pro Ala Ala Arg Pro Thr Pro Pro Thr Cys Tyr Ser Arg  
86 20 25 30  
88 Met Arg Ala Leu Ser Gln Glu Ile Thr Arg Asp Phe Asn Leu Leu  
89 35 40 45  
91 Gln Val Ser Glu Pro Ser Glu Pro Cys Val Arg Tyr Leu Pro Arg  
92 50 55 60  
94 Leu Tyr Leu Asp Ile His Asn Tyr Cys Val Leu Asp Lys Leu Arg  
95 65 70 75  
97 Asp Phe Val Ala Ser Pro Pro Cys Trp Lys Val Ala Gln Val Asp  
98 80 85 90  
100 Ser Leu Lys Asp Lys Ala Arg Lys Leu Tyr Thr Ile Met Asn Ser  
101 95 100 105  
103 Phe Cys Arg Arg Asp Leu Val Phe Leu Leu Asp Asp Cys Asn Ala  
104 110 115 120  
106 Leu Glu Tyr Pro Ile Pro Val Thr Thr Val Leu Pro Asp Arg Gln  
107 125 130 135  
109 Arg  
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113 <211> LENGTH: 579  
114 <212> TYPE: DNA  
115 <213> ORGANISM: Homo Sapien  
117 <400> SEQUENCE: 3  
118 caccaaagac actacctctg ttgctgtgc tgggttgtt ggtatagcc 50  
120 tggcctctgg cagtacagtc cgcgcgcgc acctgctact ctcggatgct 100  
122 gaccctgagc cgtgagatca tggcagactt ccagagcctg caggcttcag 150  
124 agcctgagga ttccctgtgtg aggtacttgc cccggcttta cctggacatc 200  
126 cataactact gtgtgtggc caagctgaga gacttcgtgg cttctcctca 250  
128 gtgctggaaatggccgaatggacactt gaaggacaga gtgcggaaagc 300  
130 tgtataccat catgaactcc ttctgcagggc gggacttggt attcctctca 350  
132 gatgactgca gtgccttaga agacccaatt cccgaggcca cgggtctcc 400  
134 agactggcag agctaaggcag gtggaccaga agaacaaccc agaggctga 450  
136 agctgggcca gttgtccaga gttacacccc ccacacacac acccaggtct 500  
138 acttttagtg ccactgttag acctgccaca tgtctctagc ttctgaaaca 550  
140 ccagtgggg tcctacact gagcatgt 579  
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143 <211> LENGTH: 136  
144 <212> TYPE: PRT  
145 <213> ORGANISM: Homo Sapien  
147 <400> SEQUENCE: 4  
148 Lys Thr Leu Pro Leu Leu Leu Leu Val Val Val Val Ile Ala  
149 1 5 10 15  
151 Trp Pro Leu Ala Val Gln Ser Ala Pro Pro Thr Cys Tyr Ser Arg

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|     |   |     |     |
|-----|---|-----|-----|
| 152 | 20  | 25  | 30  |
| 154 | Met Leu Thr Leu Ser Arg Glu Ile Met Ala Asp Phe Gln Ser Leu |     |     |
| 155 | 35  | 40  | 45  |
| 157 | Gln Ala Ser Glu Pro Glu Asp Ser Cys Val Arg Tyr Leu Pro Arg |     |     |
| 158 | 50  | 55  | 60  |
| 160 | Leu Tyr Leu Asp Ile His Asn Tyr Cys Val Leu Ala Lys Leu Arg |     |     |
| 161 | 65  | 70  | 75  |
| 163 | Asp Phe Val Ala Ser Pro Gln Cys Trp Lys Met Ala Glu Val Asp |     |     |
| 164 | 80  | 85  | 90  |
| 166 | Thr Leu Lys Asp Arg Val Arg Lys Leu Tyr Thr Ile Met Asn Ser |     |     |
| 167 | 95  | 100 | 105 |
| 169 | Phe Cys Arg Arg Asp Leu Val Phe Leu Ser Asp Asp Cys Ser Ala |     |     |
| 170 | 110   | 115 | 120 |
| 172 | Leu Glu Asp Pro Ile Pro Glu Ala Thr Gly Pro Pro Asp Trp Gln |     |     |
| 173 | 125   | 130 | 135 |
| 175 | Ser   |     |     |

**VERIFICATION SUMMARY**  
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